

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wang, Elizabeth A.  
Rosen, Vicki A.  
Wozney, John M.
- (ii) TITLE OF INVENTION: Novel BMP Products
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
(B) STREET: 87 CAMBRIDGEPARK DRIVE  
(C) CITY: CAMBRIDGE  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: KAPINOS, ELLEN J.  
(B) REGISTRATION NUMBER: 32,245  
(C) REFERENCE/DOCKET NUMBER: GI5160C
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617-876-1170  
(B) TELEFAX: 617-876-5851

FOI b 7 E O S S E 4 0 6 6 0

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: BOS TAURUS
- (vii) IMMEDIATE SOURCE:

(A) LIBRARY: ~~XXXXXXXXXX~~ ~~XXXXXXXXXX~~ LINE GENOMIC IN LAMBDA J1 ~~XXXXXXXXXX~~  
(B) CLONE: LAMBDA BP-21

) POSITION IN GENOME:  
(C) UNITS: bp

x) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..390

ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 46..387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
5 CAC GAT GGG AAA GGA CAC CCT CTC CAC AGA AGA GAA AAG CGG CAA           48
  His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln           1
                               -10                                 -5
A AAA CAC AAA CAG CGG AAA CGC CTC AAG TCC AGC TGT AAG AGA CAC           96
a Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His           15
                               5                                 10                                 15
TCT TTA TAT GTG GAC TTC AGT GAT GTG GGG TGG AAT GAC TGG ATC GTT          144
Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val          30
                               20                                 25                                 30
GCA CCG CCG GGG TAT CAT GCC TTT TAC TGC CAT GGG GAG TGC CCT TTT          192
Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe          45
                               35                                 40                                 45
CCC CTG GCC GAT CAC CTT AAC TCC ACG AAT CAT GCC ATT CTC CAA ACT          240
Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr          65
                               50                                 55                                 60                                 65
CTG GTC AAC TCA GTT AAC TCT AAG ATT CCC AAG GCA TGC TGT GTC CCA          288
Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro          75
                               70                                 75                                 80
ACA GAG CTC AGC GCC ATC TCC ATG CTG TAC CTT GAT GAG AAT GAG AAG          336
Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys          85
                               85                                 90                                 95
GTG GTA TTA AAG AAC TAT CAG GAC ATG GTT GTC GAG GGT TGT GGG TGT          384
Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys          100
                               105                                 110
CGT TAGCACAGCA AAATAAAATA TAAATATATA TATATATATA TTAGAAAAC          437
Arg
115
AGCAAAAAAA TCAAGTTGAC ACTTTAATAT TTCCAATGA AGACTTTATT TATGGAATGG          497
AATGGAGAAA AAGAAAAACA CAGCTATTTT GAAACTATA TTTATATCTA CCGAAAAGAA          557
GTTGGGAAAA CAAATATTTT AATCAGAGAA TTATT                                  592
```

INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln  
-15 -10 -5 1

Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His  
5 10 15

Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val  
20 25 30

Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe  
35 40 45

Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr  
50 55 60 65

Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro  
70 75 80

Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys  
85 90 95

Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys  
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1607 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (G) CELL TYPE: Osteosarcoma Cell Line
- (H) CELL LINE: U-20S

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U20S cDNA in Lambda GT10

(B) CLONE: **[REDACTED]** U20S-39

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 356..1546

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1202..1543

(ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 14..1607

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 356..424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT 60  
AAATTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT 120  
CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTCACAGC 180  
GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG 240  
GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA 300  
ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG 358  
Met  
-282  
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC 406  
Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu  
-280 -275 -270  
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC 454  
Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe  
-265 -260 -255 -250  
GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC 502  
Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val  
-245 -240 -235  
CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG 550  
Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln  
-230 -225 -220  
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC 598  
Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp  
-215 -210 -205  
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC 646

Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp	His		
-200																	
CGG	TTG	GAG	AGG	GCA	GCC	AGC	CGA	GCC	AAC	ACT	GTG	CGC	AGC	TTC	CAC		694
Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	His		
-185																	-170
CAT	GAA	GAA	TCT	TTG	GAA	GAA	CTA	CCA	GAA	ACG	AGT	GGG	AAA	ACA	ACC		742
His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	Thr		
																	-155
CGG	AGA	TTC	TTC	TTT	AAT	TTA	AGT	TCT	ATC	CCC	ACG	GAG	GAG	TTT	ATC		790
Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	Ile		
																	-140
ACC	TCA	GCA	GAG	CTT	CAG	GTT	TTC	CGA	GAA	CAG	ATG	CAA	GAT	GCT	TTA		838
Thr	Ser	Ala	Glu	Leu	Gln	Val	Phe	Arg	Glu	Gln	Met	Gln	Asp	Ala	Leu		
																	-125
CGA	AAC	AAT	AGC	AGT	TTC	CAT	CAC	CGA	ATT	AAT	ATT	TAT	GAA	ATC	ATA		886
Gly	Asn	Asn	Ser	Ser	Phe	His	His	Arg	Ile	Asn	Ile	Tyr	Glu	Ile	Ile		
																	-110
AAA	CCT	GCA	ACA	GCC	AAC	TCG	AAA	TTC	CCC	GTG	ACC	AGA	CTT	TTG	GAC		934
Lys	Pro	Ala	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	Asp		-90
-105																	
ACC	AGG	TTG	GTG	AAT	CAG	AAT	GCA	AGC	AGG	TGG	GAA	AGT	TTT	GAT	GTC		982
Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Ser	Phe	Asp	Val		
																	-75
ACC	CCC	GCT	GTG	ATG	CGG	TGG	ACT	GCA	CAG	GGA	CAC	GCC	AAC	CAT	GGA		1030
Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	Gly		
																	-60
ITC	GTG	GTG	GAA	GTG	GCC	CAC	TTG	GAG	GAG	AAA	CAA	GGT	GTC	TCC	AAG		1078
Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	Lys		
																	-45
AGA	CAT	GTT	AGG	ATA	AGC	AGG	TCT	TTG	CAC	CAA	GAT	GAA	CAC	AGC	TGG		1126
Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser	Trp		
																	-30
ICA	CAG	ATA	AGG	CCA	TTG	CTA	GTA	ACT	TTT	GGC	CAT	GAT	GGA	AAA	GGG		1174
Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys	Gly		
																	-10
CAT	CCT	CTC	CAC	AAA	AGA	GAA	AAA	CGT	CAA	GCC	AAA	CAC	AAA	CAG	CGG		1222
His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln	Arg		
																	-5
AAA	CGC	CTT	AAG	TCC	AGC	TGT	AAG	AGA	CAC	CCT	TTG	TAC	GTG	GAC	TTC		1270
Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe		
																	10
																	15
																	20
AGT	GAC	GTG	GGG	TGG	AAT	GAC	TGG	ATT	GTG	GCT	CCC	CCG	GGG	TAT	CAC		1318
Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His		
																	25
																	30
																	35
GCC	TTT	TAC	TGC	CAC	GGA	GAA	TGC	CCT	TTT	CCT	CTG	GCT	GAT	CAT	CTG		1366

Ala	Phe	Tyr	Cys	His	Gly	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu			
40					45			50					55			
AC	TCC	ACT	AAT	CAT	GCC	ATT	GTT	CAG	ACG	TTG	GTC	AAC	TCT	GTT	AAC	1414
Asn	Ser	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	
				60				65						70		
ACT	AAG	ATT	CCT	AAG	GCA	TGC	TGT	GTC	CCG	ACA	GAA	CTC	AGT	GCT	ATC	1462
Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	
			75					80						85		
TCG	ATG	CTG	TAC	CTT	GAC	GAG	AAT	GAA	AAG	GTT	GTA	TTA	AAG	AAC	TAT	1510
Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	
		90					95							100		
TAG	GAC	ATG	GTT	GTG	GAG	GGT	TGT	GGG	TGT	CGC	TAGTACAGCA AAATTAAATA				1563	
Gln	Asp	Met	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg						
	105					110				115						
ATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA															1607	

2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Ala	Gly	Thr	Arg	Cys	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	Val	
-282		-280					-275						-270			
Leu	Leu	Gly	Gly	Ala	Ala	Gly	Leu	Val	Pro	Glu	Leu	Gly	Arg	Arg	Lys	
-265						-260						-255				
he	Ala	Ala	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Ser	Gln	Pro	Ser	Asp	Glu	
-250						-245					-240				-235	
Val	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	Phe	Gly	Leu	Lys	
				-230						-225					-220	
Gln	Arg	Pro	Thr	Pro	Ser	Arg	Asp	Ala	Val	Val	Pro	Pro	Tyr	Met	Leu	
			-215					-210							-205	
asp	Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp	
		-200					-195						-190			
His	Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	
		-185					-180						-175			
His	His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	
-170					-165						-160					-155
Thr	Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	
				-150						-145					-140	

Ile Thr Ser Ala Glu Leu Val Phe Arg Glu Gln Met Asp Ala  
 -135 -130 -125

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile  
 -120 -115 -110

Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu  
 -105 -100 -95

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp  
 -90 -85 -80 -75

Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His  
 -70 -65 -60

Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser  
 -55 -50 -45

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser  
 -40 -35 -30

Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys  
 -25 -20 -15

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln  
 -10 -5 1 5  
 +262  
 243

Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp  
 10 15 17 20  
 +262  
 299

Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr  
 25 30 35

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His  
 40 45 50

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val  
 55 60 65 70

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala  
 75 80 85

Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn  
 90 95 100

Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg  
 105 110 114  
 382  
 396

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (G) CELL TYPE: Osteosarcoma Cell Line
- (H) CELL LINE: U-2OS

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2OS cDNA in Lambda gt10
- (B) CLONE: Lambda U2OS-3

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 403..1629

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1279..1626

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 9..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA 60  
GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG 120  
AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC 180  
ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG 240  
CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC 300  
GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA 360  
TCATGGACTG TTATTATATG CCTTGTTTTT TGTC AAGACA CC ATG ATT CCT GGT 414  
Met Ile Pro Gly  
-292 -290  
AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC 462  
Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly  
-285 -280 -275  
GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC 510  
Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala  
-270 -265 -260  
GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG 558  
Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu  
-255 -250 -245  
CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC 606  
Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg



-240		-215		-230		-225	
CGC CGC CCG CAG CCT AGC AAG AGT GCC GTC ATT CCG GAC TAC ATG CGG							654
Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg							
		-220		-215		-210	
GAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAA GAG CAG ATC CAC							702
Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu Glu Gln Ile His							
		-205		-200		-195	
AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC AGC CGG GCC AAC ACC							750
Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser Arg Ala Asn Thr							
		-190		-185		-180	
GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC CCA GGG ACC							798
Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile Pro Gly Thr							
		-175		-170		-165	
AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT							846
Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile Pro							
		-160		-155		-150	-145
JAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG							894
Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln							
		-140		-135		-130	
GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT							942
Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile							
		-125		-120		-115	
TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC							990
Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile							
		-110		-105		-100	
ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG							1038
Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp							
		-95		-90		-85	
GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG							1086
Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys							
		-80		-75		-70	-65
CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT							1134
Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr							
		-60		-55		-50	
CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA							1182
Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln							
		-45		-40		-35	
GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC							1230
Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly							
		-30		-25		-20	
CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT							1278
His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg							
		-15		-10		-5	
AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC							1326
Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys							

1	5	10	15	
CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC				1374
Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp	20	25	30	
TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC				1422
Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp	35	40	45	
TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT				1470
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile	50	55	60	
GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT				1518
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys	65	70	75	80
TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG				1566
Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu	85	90	95	
TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA				1614
Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly	100	105	110	
TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC				1666
Cys Gly Cys Arg	115			
CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC				1726
ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAATAA AATGGAAAAA				1786
ATCCCTAAAC ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT				1846
TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG				1906
AGTCATTATT TTAAAAAATA AAAAAAACT CTAGAGTCGA CGGAATTC				1954

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ile	Pro	Gly	Asn	Arg	Met	Leu	Met	Val	Val	Leu	Leu	Cys	Gln	Val
-292		-290					-285						-280		
Leu	Leu	Gly	Gly	Ala	Ser	His	Ala	Ser	Leu	Ile	Pro	Glu	Thr	Gly	Lys
	-275					-270						-265			
Lys	Lys	Val	Ala	Glu	Ile	Gln	Gly	His	Ala	Gly	Gly	Arg	Arg	Ser	Gly
-260					-255					-250					-245

Gln Ser His Glu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met  
 -240 -235 -230

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro  
 -225 -220 -215

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu  
 -210 -205 -200

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser  
 -195 -190 -185

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn  
 -180 -175 -170 -165

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu  
 -160 -155 -150

Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu  
 -145 -140 -135

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His  
 -130 -125 -120

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro  
 -115 -110 -105

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn  
 -100 -95 -90 -85

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp  
 -80 -75 -70

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His  
 -65 -60 -55

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg  
 -50 -45 -40

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu  
 -35 -30 -25

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg  
 -20 -15 -10 -5

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys  
 1 5 10

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val  
 15 20 25

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr  
 30 35 40

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr  
 45 50 55 60

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile  
 65 70 75

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu  
80 85 90

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met  
95 100 105

Val Val Glu Gly Cys Gly Cys Arg  
110 115

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